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at least two consensus sequences, said at least two consensus sequences corresponding to conserved sequences identified in said organism or group of organisms, at least half of each of said consensus sequences being kept constant in the set of promoter sequences, the at least two consensus sequences, when the selected organism or group of organisms is prokaryotic, being selected from the group consisting of TATAAT, TTGACA and an activator binding site upstream of the TATAAT sequence, when the selected organism or group of organisms is eukaryotic, being selected from the group consisting of a TATA-box and a UAS upstream of said TATA-box and, between said consensus sequences or flanking at least one of said consensus sequences, at least one nucleotide spacer sequence, at least part of which, relative to the corresponding spacer sequence of the identified promoter, is varied by random incorporation of nucleotides that are selected from the group consisting of the nucleobases A, T, C and G.

REMARKS

Applicants gratefully acknowledge the telephonic interview granted by the Examiner on September 26, 2002 to Applicants' representatives. As discussed during that interview, Applicants herein provide the foregoing amendment to clarify the subject matter of the present invention. Applicants respectfully submit that the amendment does not add new matter.

REQUEST FOR ALLOWANCE

For at least the reasons detailed above, Applicants respectively submit that all of the claims in the application are patentable. Favorable consideration, entry of this amendment, and issuance of a notice of allowance are respectively requested.